

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=10; day=31; hr=13; min=10; sec=55; ms=859;  
]

=====

Application No: 10552786 Version No: 2.0

**Input Set:****Output Set:**

**Started:** 2008-09-29 19:39:18.196  
**Finished:** 2008-09-29 19:39:20.020  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 824 ms  
**Total Warnings:** 104  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 130  
**Actual SeqID Count:** 130

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

**Input Set:**

**Output Set:**

**Started:** 2008-09-29 19:39:18.196  
**Finished:** 2008-09-29 19:39:20.020  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 824 ms  
**Total Warnings:** 104  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 130  
**Actual SeqID Count:** 130

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

# SEQUENCE LISTING

<110> DEPERTHES, David  
CLOUTIER, Sylvain

<120> INHIBITOR PROTEINS OF A PROTEASE AND USE THEREOF

<130> KZY-003US

<140> 10552786

<141> 2006-07-25

<150> PCT/IB2004/001040

<151> 2004-04-05

<150> US 60/460345

<151> 2003-04-04

<160> 130

<170> PatentIn version 3.5

<210> 1

<211> 1239

<212> DNA

<213> Artificial sequence

<220>

<223> DNA Sequence ACT variants : MD 820

<400> 1

atgagaggat cccatcacca tcaccatcac tctagacacc ctaacagccc acttgacgag	60
gagaatctga ccaggagaa ccaagaccga gggacacacg tggacctcg attagcctcc	120
gccaacgtgg acttcgcttt cagcctgtac aagcagttag tcctgaaggc ccctgataag	180
aatgtcatct tctcccact gagcatctcc accgccttgg ccttcctgtc tctgggggcc	240
cataatacca ccctgacaga gattctcaaa ggcctcaagt tcaacctcac ggagacttct	300
gaggcagaaa ttcaccagag ctccagcac ctctgcgca ccctcaatca gtccagcgat	360
gagctgcagc tgagtatggg aaatgccatg tttgtcaaag agcaactcag tctgctggac	420
aggttcacgg aggatgccaa gaggctgtat ggctccgagg cctttgccac tgactttcag	480
gactcagctg cagctaagaa gctcatcaac gactacgtga agaatggaac tagggggaaa	540
atcacagatc tgatcaagga ccttgactcg cagacaatga tggtcctggg gaattacatc	600
ttcttttaaag ccaaattggga gatgcccttt gacccccaag atactcatca gtcaaggttc	660
tacttgagca agaaaaagtg ggtaatggtg cccatgatga gtttgcatca cctgactata	720
ccttacttcc gggacgagga gctgtcctgc accgtggtgg agctgaagta cacaggcaat	780

gccagcgcac ttttcatacct ccctgatcaa gacaagatgg aggaagtgga agccatgctg 840  
ctcccagaga ccctgaagcg gtggagagac tctctggagt tcagagagat aggtgagctc 900  
tacctgccaa agttttccat ctcgagggac tataacctga acgacatact tctccagctg 960  
ggcattgagg aagccttcac cagcaaggct gacctgtcag ggatcacagg ggccaggaac 1020  
ctagcagtct ccaggtggt ccataaggct gtgcttgatg tatttgagga gggcacagaa 1080  
gcatctgctg ccaccgcggt caaaatcacc ctccgttctc gagcagtgga gacgcgtacc 1140  
attgtgcgtt tcaacaggcc cttcctgatg atcattgtcc ctacagacac ccagaacatc 1200  
ttcttcatga gcaaagtcac caatcccaag caagcctaa 1239

<210> 2

<211> 412

<212> PRT

<213> Artificial sequence

<220>

<223> Protein Sequence ACT variants : MD 820

<400> 2

Met Arg Gly Ser His His His His His His Ser Arg His Pro Asn Ser  
1 5 10 15

Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr  
20 25 30

His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser  
35 40 45

Leu Tyr Lys Gln Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe  
50 55 60

Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala  
65 70 75 80

His Asn Thr Thr Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu  
85 90 95

Thr Glu Thr Ser Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu  
100 105 110

Arg Thr Leu Asn Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn

115

120

125

Ala Met Phe Val Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu  
130 135 140

Asp Ala Lys Arg Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln  
145 150 155 160

Asp Ser Ala Ala Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly  
165 170 175

Thr Arg Gly Lys Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr  
180 185 190

Met Met Val Leu Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met  
195 200 205

Pro Phe Asp Pro Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys  
210 215 220

Lys Lys Trp Val Met Val Pro Met Met Ser Leu His His Leu Thr Ile  
225 230 235 240

Pro Tyr Phe Arg Asp Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys  
245 250 255

Tyr Thr Gly Asn Ala Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys  
260 265 270

Met Glu Glu Val Glu Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp  
275 280 285

Arg Asp Ser Leu Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys  
290 295 300

Phe Ser Ile Ser Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu  
305 310 315 320

Gly Ile Glu Glu Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr  
325 330 335

Gly Ala Arg Asn Leu Ala Val Ser Gln Val Val His Lys Ala Val Leu  
340 345 350

Asp Val Phe Glu Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys  
355 360 365

Ile Thr Leu Arg Ser Arg Ala Val Glu Thr Arg Thr Ile Val Arg Phe  
370 375 380

Asn Arg Pro Phe Leu Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile  
385 390 395 400

Phe Phe Met Ser Lys Val Thr Asn Pro Lys Gln Ala  
405 410

<210> 3

<211> 1239

<212> DNA

<213> Artificial sequence

<220>

<223> DNA Sequence ACT variant : MD 62

<400> 3

atgagaggat cccatcacca tcaccatcac tctagacacc ctaacagccc acttgacgag	60
gagaatctga ccaggagaa ccaagaccga gggacacacg tggacctcgg attagcctcc	120
gccaacgtgg acttcgcttt cagcctgtac aagcagttag tcctgaaggc cctgataag	180
aatgtcatct tctcccact gagcatctcc accgccttgg ctttcctgtc tctgggggcc	240
cataatacca cctgacaga gattctcaaa ggcctcaagt tcaacctcac ggagacttct	300
gaggcagaaa ttcaccagag cttccagcac ctctgcgc caactcaatca gtccagcgat	360
gagctgcagc tgagtatggg aaatgccatg tttgtcaaag agcaactcag tctgctggac	420
aggttcacgg aggatgccaa gaggetgtat ggctccgagg cctttgccac tgactttcag	480
gactcagctg cagctaagaa gctcatcaac gactacgtga agaattggaac tagggggaaa	540
atcacagatc tgatcaagga ccttgactcg cagacaatga tggctcctggg gaattacatc	600
ttcttttaaag ccaaattgga gatgcccttt gacccccaag atactcatca gtcaagggtc	660
tacttgagca agaaaaagtg ggtaatgggtg cccatgatga gtttgcatca cctgactata	720
ccttacttcc gggacgagga gctgtcctgc accgtgggtg agctgaagta cacaggcaat	780
gccagcgcac tcttcatacct ccctgatcaa gacaagatgg aggaagtgga agccatgctg	840
ctcccagaga cctgaagcg gtggagagac tctctggagt tcagagagat aggtgagctc	900

```

tacctgccaa agttttccat ctcgagggac tataacctga acgacatact tctccagctg      960
ggcattgagg aagccttcac cagcaaggct gacctgtcag ggatcacagg ggccaggaa      1020
ctagcagtct cccaggtggt ccataaggct gtgcttgatg tatttgagga gggcacagaa      1080
gcatctgctg ccaccgcggt caaaatcacc aggaggtcta tcgatgtgga gacgcgtacc      1140
attgtgcgtt tcaacaggcc cttcctgatg atcattgtcc ctacagacac ccagaacatc      1200
ttcttcatga gcaaagtcac caatcccaag caagcctaa      1239

```

<210> 4

<211> 412

<212> PRT

<213> Artificial sequence

<220>

<223> Protein Sequence ACT variant : MD 62

<400> 4

```

Met Arg Gly Ser His His His His His Ser Arg His Pro Asn Ser
1              5              10              15

```

```

Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr
                20              25              30

```

```

His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser
        35              40              45

```

```

Leu Tyr Lys Gln Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe
    50              55              60

```

```

Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala
65              70              75              80

```

```

His Asn Thr Thr Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu
        85              90              95

```

```

Thr Glu Thr Ser Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu
        100             105             110

```

```

Arg Thr Leu Asn Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn
        115             120             125

```

```

Ala Met Phe Val Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu
    130             135             140

```



Asp Ala Lys Arg Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln  
145 150 155 160

Asp Ser Ala Ala Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly  
165 170 175

Thr Arg Gly Lys Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr  
180 185 190

Met Met Val Leu Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met  
195 200 205

Pro Phe Asp Pro Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys  
210 215 220

Lys Lys Trp Val Met Val Pro Met Met Ser Leu His His Leu Thr Ile  
225 230 235 240

Pro Tyr Phe Arg Asp Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys  
245 250 255

Tyr Thr Gly Asn Ala Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys  
260 265 270

Met Glu Glu Val Glu Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp  
275 280 285

Arg Asp Ser Leu Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys  
290 295 300

Phe Ser Ile Ser Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu  
305 310 315 320

Gly Ile Glu Glu Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr  
325 330 335

Gly Ala Arg Asn Leu Ala Val Ser Gln Val Val His Lys Ala Val Leu  
340 345 350

Asp Val Phe Glu Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys  
355 360 365

Ile Thr Arg Arg Ser Ile Asp Val Glu Thr Arg Thr Ile Val Arg Phe  
 370 375 380

Asn Arg Pro Phe Leu Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile  
 385 390 395 400

Phe Phe Met Ser Lys Val Thr Asn Pro Lys Gln Ala  
 405 410

<210> 5

<211> 1239

<212> DNA

<213> Artificial sequence

<220>

<223> DNA Sequence ACT variant : MD 83

<400> 5

atgagaggat cccatcacca tcaccatcac tctagacacc ctaacagccc acttgacgag	60
gagaatctga cccaggagaa ccaagaccga gggacacacg tggacctcgg attagcctcc	120
gccaacgtgg acttcgcttt cagcctgtac aagcagttag tcctgaaggc ccctgataag	180
aatgtcatct tctccccact gagcatctcc accgccttgg ccttcctgtc tctggggggc	240
cataatacca ccctgacaga gattctcaaa ggcctcaagt tcaacctcac ggagacttct	300
gaggcagaaa ttcaccagag ctccagcac ctccctgcgc cctcaatca gtccagcgat	360
gagctgcagc tgagtatggg aaatgccatg tttgtcaaag agcaactcag tctgctggac	420
aggttcacgg aggatgccaa gaggctgtat ggctccgagg cctttgccac tgactttcag	480
gactcagctg cagctaagaa gctcatcaac gactacgtga agaatggaac tagggggaaa	540
atcacagatc tgatcaagga ccttgactcg cagacaatga tggtcctggg gaattacatc	600
ttcttttaaag ccaaattgga gatgcccttt gacccccaaag atactcatca gtcaaggttc	660
tacttgagca agaaaaagtg ggtaatgggtg cccatgatga gtttgcatca cctgactata	720
ccttacttcc gggacgagga gctgtcctgc accgtgggtgg agctgaagta cacaggcaat	780
gccagcgcac tcttcatacct ccctgatcaa gacaagatgg aggaagtgga agccatgctg	840
ctcccagaga ccctgaagcg gtggagagac tctctggagt tcagagagat aggtgagctc	900
tacctgccaa agttttccat ctcgagggac tataacctga acgacatact tctccagctg	960
ggcattgagg aagccttcac cagcaaggct gacctgtcag ggatcacagg ggccaggaa	1020
ctagcagtct cccaggtggg ccataaggct gtgcttgatg tatttgagga gggcacagaa	1080

gcacatctgctg ccaccgcggt caaaatcagg gggagatctg agttagtgga gacgcgtacc 1140  
attgtgcgtt tcaacaggcc cttcctgatg atcattgtcc ctacagacac ccagaacatc 1200  
ttcttcatga gcaaagtcac caatcccaag caagcctaa 1239

<210> 6  
<211> 412  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Protein Sequence ACT variant : MD 83

<400> 6

Met Arg Gly Ser His His His His His His Ser Arg His Pro Asn Ser  
1 5 10 15

Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr  
20 25 30

His Val Asp Leu Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser  
35 40 45

Leu Tyr Lys Gln Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe  
50 55 60

Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala  
65 70 75 80

His Asn Thr Thr Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu  
85 90 95

Thr Glu Thr Ser Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu  
100 105 110

Arg Thr Leu Asn Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn  
115 120 125

Ala Met Phe Val Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu  
130 135 140

Asp Ala Lys Arg Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln  
145 150 155 160

Asp Ser Ala Ala Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly		
165	170	175
Thr Arg Gly Lys Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr		
180	185	190
Met Met Val Leu Val Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met		
195	200	205
Pro Phe Asp Pro Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys		
210	215	220
Lys Lys Trp Val Met Val Pro Met Met Ser Leu His His Leu Thr Ile		
225	230	235 240
Pro Tyr Phe Arg Asp Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys		
245	250	255
Tyr Thr Gly Asn Ala Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys		
260	265	270
Met Glu Glu Val Glu Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp		
275	280	285
Arg Asp Ser Leu Glu Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys		
290	295	300
Phe Ser Ile Ser Arg Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu		
305	310	315 320
Gly Ile Glu Glu Ala Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr		
325	330	335
Gly Ala Arg Asn Leu Ala Val Ser Gln Val Val His Lys Ala Val Leu		
340	345	350
Asp Val Phe Glu Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys		
355	360	365
Ile Arg Gly Arg Ser Glu Leu Val Glu Thr Arg Thr Ile Val Arg Phe		
370	375	380

Asn	Arg	Pro	Phe	Leu	Met	Ile	Ile	Val	Pro	Thr	Asp	Thr	Gln	Asn	Ile
385					390				395					400	

Phe	Phe	Met	Ser	Lys	Val	Thr	Asn	Pro	Lys	Gln	Ala
				405				410			

<210> 7  
 <211> 1239  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> DNA Sequence ACT variant : MD 67

<400> 7	
atgagaggat cccatcacca tcaccatcac tctagacacc ctaacagccc acttgacgag	60
gagaatctga ccaggagaa ccaagaccga gggacacacg tggacctcgg attagcctcc	120
gccaacgtgg acttcgcttt cagcctgtac aagcagttag tcctgaaggc cctgataag	180
aatgtcatct tctccccact gagcatctcc accgccttgg ccttcctgtc tctgggggcc	240
cataatacca cctgacaga gattctcaaa ggcctcaagt tcaacctcac ggagacttct	300
gaggcagaaa ttcaccagag cttccagcac ctctgcgcga ccctcaatca gtccagcgat	360
gagctgcagc tgagtatggg aaatgccatg tttgtcaaag agcaactcag tctgctggac	420
aggttcacgg aggatgccaa gaggetgtat ggctccgagg cctttgccac tgactttcag	480
gactcagctg cagctaagaa gctcatcaac gactacgtga agaatggaac tagggggaaa	540
atcacagatc tgatcaagga ccttgactcg cagacaatga tggtcctggg gaattacatc	600
ttcttttaaag ccaaattgga gatgcccttt gacccccaaag atactcatca gtcaagggtc	660
tacttgagca agaaaaagtg ggtaatggtg cccatgatga gtttgcatca cctgactata	720
ccttacttcc gggacgagga gctgtcctgc accgtggtgg agctgaagta cacaggcaat	780
gccagcgcac tcttcatect ccctgatcaa gacaagatgg aggaagtgga agccatgctg	